



Release 3.1A John F. Collins, Biocomputing Research Unit.
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Msearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 28 17:36:04 1999; Maspar time 4711.84 Seconds

1403.358 Million cell updates/sec

Tabular output not generated.

Title: >US-09-327-230-1

Description: (1-2822) From US09327230.seq

Perfect Score: 2822

N.A. Sequence: 1 gcaacgcacacacagcga.....ttccagtttggttcgq 2822

Comp: cgttcgtgtgtctgtcgt.....aagtcacacacacacaccc

Scoring table: TABLE default

Gap 6

Mismatch STD: Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 08

Listing first 45 summaries

Database: emb1_est158

1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2

Database: genbank_est11

8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
17:gb_est18 18:gb_est19 19:gb_est20 20:gb_est21
21:gb_est22 22:gb_est23 23:gb_est24 24:gb_est25
25:gb_est26 26:gb_est27 27:gb_est28 28:gb_est29
29:gb_est30 30:gb_est31 31:gb_est32 32:gb_est33 33:gb_est34
34:gb_est35 35:gb_est36 36:gb_est37 37:gb_est38 38:gb_est39
39:gb_est40 40:gb_est41 41:gb_est42 42:gb_est43

Statistics: Mean 12.348; Variance 2.671; scale 4.623

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	58	2.1	252	17	AA754459	97SN1787 Rice Immature	4.07e-49
2	59	2.1	252	17	AA754459	97SN1787 Rice Immature	1.04e-50
3	53	1.9	247	17	AA754458	97SN1784 Rice Immature	2.90e-41
4	49	1.7	247	17	AA754458	97SN1784 Rice Immature	3.91e-35
5	44	1.6	656	27	AI467722	486015E01.x2 486 - lea	1.06e-27
6	44	1.6	697	27	AI444709	486015E01.x5 486 - lea	1.06e-27
7	39	1.4	2275	20	AF034173	AF034173 Human mRNA (T	1.40e-20
8	37	1.3	2275	20	AF034173	AF034173 Human mRNA (T	7.77e-18
9	27	1.0	250	16	AA633452	np62b07.s1 NCI.CGAP.Br	2.38e-05
10	27	1.0	301	20	AA846497	a185901.s1 Soares_Para	2.38e-05

C	11	29	1.0	308	27	AI469425	tm08f07.x1 NCI.CGAP.Co	1.20e-07
C	12	27	1.0	311	18	AA810844	oa76e12.s1 NCI.CGAP.Co	2.38e-05
C	13	27	1.0	315	10	AA262545	zs17g05.r1 NCI.CGAP.Co	2.38e-05
C	14	27	1.0	321	34	W29651	mc07b04.r1 Soares.mous	2.38e-05
C	15	27	1.0	372	42	AA445618	GSSrc00106 Trypanosoma	2.38e-05
C	16	28	1.0	373	37	B22796	P22E3TF IGF Arabidops1	1.75e-06
C	17	27	1.0	405	18	AA808125	oc39e10.s1 NCI.CGAP.Co	2.38e-05
C	18	27	1.0	411	33	N70046	ca70b08.s1 Soares.feta	2.38e-05
C	19	27	1.0	417	13	AA418029	zv94h03.s1 Soares.NhM	2.38e-05
C	20	27	1.0	427	18	AA811626	ob74d01.s2 NCI.CGAP.Co	2.38e-05
C	21	27	1.0	441	40	AA176938	HS_3208.A1 C11.MR.CIT	2.38e-05
C	22	27	1.0	464	42	AA425011	C11B1-ET-2563M9.TR.CIT	2.38e-05
C	23	27	1.0	467	26	AI371756	ta34c07.x1 NCI.CGAP.Co	2.38e-05
C	24	27	1.0	483	25	AI354761	qt51e01.x1 Soares.feta	2.38e-05
C	25	27	1.0	482	40	AA240278	CIT-HSP-2385J15.TR.1.C	2.38e-05
C	26	27	1.0	508	38	AA003489	CIT-HSP-2320H6.TR.CIT	2.38e-05
C	27	27	1.0	510	9	AA205305	zg79a04.s1 Strataene	2.38e-05
C	28	28	1.0	587	40	AA273443	nbx0030109T CGU1 Rice	1.75e-06
C	29	27	1.0	592	18	AA819944	ETN228 Trypanosoma bru	2.38e-05
C	30	28	1.0	659	37	B96033	F22E3TFB IGF Arabidops	1.75e-06
C	31	25	0.9	223	25	AI301358	q027h08.x1 NCI.CGAP.K1	3.50e-04
C	32	26	0.9	300	15	C51599	CS1599.yuji Kohara ump	3.00e-04
C	33	26	0.9	323	30	R32871	yh73c09.r1 Soares.plac	3.00e-04
C	34	26	0.9	366	39	AA111879	CIT-HSP-2379J19.TR.CIT	3.00e-04
C	35	26	0.9	371	39	AA085802	HS_2270.B1.E01.MR.CIT	3.00e-04
C	36	26	0.9	428	31	H47789	YP80e02.r1 Soares.feta	3.00e-04
C	37	26	0.9	448	39	AA084447	CSRL-13e10-u CSRL.f10	3.00e-04
C	38	26	0.9	530	37	B01598	CIT-HSP-2025J13.TF.CIT	3.00e-04
C	39	25	0.9	540	38	B69019	RPCL11-91G15.TV.RPCL11	3.50e-03
C	40	26	0.9	559	41	AA281393	AAU015749 Mouse two-cel	3.00e-04
C	41	26	0.9	584	22	AAU015749	nbx0013A16r CGU1 Rice	3.00e-04
C	42	26	0.9	623	39	AA159255	nbx0011A02r CGU1 Rice	3.00e-04
C	43	26	0.9	692	39	AA158371	HS_2028.A2.C09.T7.CIT	3.00e-04
C	44	26	0.9	725	41	AA0307139	CIT-HSP-2028E8.TFB.CIT	3.00e-04
C	45	26	0.9	734	40	B70215		

ALIGNMENTS

RESULT	1	LOCUS	1	AA754459	252 bp	mRNA	EST	20-JAN-1998
DEFINITION	97SN1787 Rice Immature Seed Lambda ZAPIT cDNA Library Oryza sativa							
CDNA clone	97SN1787, mRNA sequence.							
ACCESSION	AA754459							
NID	92801165							
VERSION	AA754459.1							
KEYWORDS	EST.							
SOURCE	Oryza sativa.							
ORGANISM	Oryza sativa.							
REFERENCE	1 (bases 1 to 252)							
AUTHORS	Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P., Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.							
TITLE	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed							
JOURNAL	Unpublished (1998)							
COMMENT	On Jan 14, 1998 this sequence version replaced gi:1797457.							

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Submitted by Baek Hye Nahm, Dept of Biological Science, Myongji University, Yongin, Korea, 448-728 bhaanmbioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
1. .252
/organism="Oryza sativa"

[illegible]

```

      /db_xref="taxon:4530"
      /map=6"
      /clone="97SN1787"
      /clone_lib="Rice Immature Seed Lambda ZAPRI cDNA library"
      /tissue_type="Immature Seed"
      /dev_stage="5 days after pollination"
      /lab_host="E. coli SOLR"
BASE COUNT    5 a          21 c        12 g         35 t       179 others
ORIGIN
Query Match           2.1%; Score 59; DB 17; Length 25Z;
Best Local Similarity 13.9%; Pred. No. 1.04e-50;
Matches   32; Conservative   114; Mismatches   80; Indels    4; Gaps    4;

Dn     24 BCGHNBWVCVCAASHGNNMSVHNCTBGTCHDDCCNVMWSMTMGTYNVMBVSGDMHYWBVB 83
      :|:::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Cp     2779 ccggaaccggaaattgttgttggaattccggtagcaacttcgaaaacccgaaatatt 2720
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

Dn     84 NTKYDVGNHTRCBSHWRETRMAHYHDYTNCBVBNND-NHM-WHBMYDBTSCMTCMWMC 141
      :||::||||::::|::||::||::||::||::||::||::||::||::||::||::||::||:
Cp     2719 tcgggatcgcgggtatcacacaaccgggtaccggaataccggaatltaaccggcttcacg 2660
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

Dn     142 WBHYNTKCTASAGMTSTINYDKSSWTWGATSBSDSKSMHGWCYSBB-VKATHYSTRAT 200
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Cp     2659 tgltcatgtacctcgatcgatctttaatatlaagttgtaacatcataaatatagtga 2601
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

Dn     201 RSYTCVRKYCYMMNTKRVEKKYHVBBGGHBDPSCKTMNMNTNKHHVMTS 250
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Cp     2600 agtgtcataactcggaatgtgataattgttgttttatataatgltcaagt 2551

```

RESULT 3
 LOCUS AA754458 247 bp mRNA
 DEFINITION 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library *Oryza sativa*
 ACCESSION CNA clone 97SN1784, mRNA sequence.
 NID AA734458
 VERSION g2801164
 KEYWORDS AA754458.1 GI:2801164
 SOURCE EST.
 ORGANISM *Oryza sativa*.
Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 Poaceae; *Oryza*.
 1 (Bases 1 to 247)
 Namb,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
 Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
 Lee,M.C. and Eun,M.Y.
 Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 Unpublished (1998)
 On Jan 14, 1998 this sequence version replaced gi:1797455.

TITLE
 JOURNAL
 COMMENT

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 Submitted by Baek Hie Namh, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 bhnahme@bioserver.myongji.ac.kr
 Seq primer: M13 Reverse Primer.
 Location/Qualifiers
 1..247

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Location/Qualifiers
1. 252
/organism="Oryza sativa"
/cultivar="Milyang23"
/note="vector: pbuinsert SK(+); Site1: EcoRI; Site2:
XhoI; Directional cDNA library inserted into lambda ZAPIII
vector at 5' end with EcoRI and 3' end with Xho I site."
```


Query Match	1.0%;	Score 29;	DB 27;	Length 308;
Best Local Similarity	79.6%;	Pred. No. 1.20e-07;		
Matches	39;	Conservative	0;	Mismatches 10; Indels 0; Gaps 0;

```
Db      242 ACCATTAAATTTACATGCCAGGAAAACATTAA'TTATAITTTAAATATACAGTAA   298
       || | ||||| || | || | ||||| || | ||||| || | ||||| || | |||||
QY     114 acaaaaaaattcacacgcctcacaacatttacaatatgatgtccaatagacactaa   170
```


